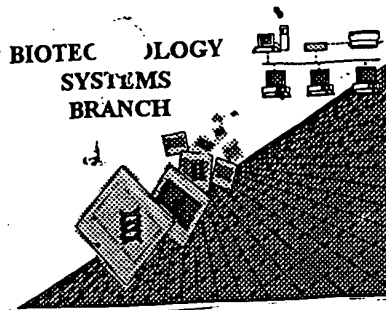


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



WA

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/869,388

Source:

PCT09

Date Processed by STIC:

11/2/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 09/869,388

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2 ☐ Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3 ☐ Misaligned Amino  
Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4 ☐ Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5 ☐ Variable Length     Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6 ☐ PatentIn 2.0  
"bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7 ☐ Skipped Sequences  
(OLD RULES)     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8 ☐ Skipped Sequences  
(NEW RULES)     Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
  
- 9 ☒ Use of n's or Xaa's  
(NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10 ☐ Invalid <213>  
Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11 ☐ Use of <220>     Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12 ☐ PatentIn 2.0  
"bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/869,388

DATE: 11/02/2001  
TIME: 14:45:23

Input Set : A:\es.txt  
Output Set: N:\CRF3\11022001\I869388.raw

Does Not Comply  
Corrected Diskette Needed

Errors on pp 1-3

5 <110> APPLICANT: Bates, Elizabeth  
6 Fournier, Nathalie  
7 Chalus, Lionel  
8 Garrone, Pierre  
10 <120> TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND  
11 METHODS  
13 <130> FILE REFERENCE: SF0977X  
C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/869,388  
C--> 16 <141> CURRENT FILING DATE: 2001-10-09  
W--> 18 <140> CURRENT APPLICATION NUMBER: 09/224,604  
C--> 19 <141> CURRENT FILING DATE: 1998-12-31  
22 <160> NUMBER OF SEQ ID NOS: 14  
24 <170> SOFTWARE: IBM PC compatible

# ERRORED SEQUENCES

137 <210> SEQ ID NO: 2  
138 <211> LENGTH: 284  
139 <212> TYPE: PRT  
140 <213> ORGANISM: homo sapiens  
142 <400> SEQUENCE: 2  
143 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro  
144 -19 -15 -10 -5  
146 Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu  
147 1 5 10  
149 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser  
150 15 20 25  
152 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala  
153 30 35 40 45  
155 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser  
156 50 55 60  
158 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg  
159 65 70 75  
161 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile  
162 80 85 90  
164 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu  
165 95 100 105  
167 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly  
168 110 115 120 125  
170 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro  
171 130 135 140  
173 Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr  
174 145 150 155  
176 Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile  
177 160 165 170  
179 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly

→ must count negative numbers.  
(Input 284, found 303)

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,388

DATE: 11/02/2001

TIME: 14:45:23

Input Set : A:\es.txt

Output Set : N:\CRF3\11022001\I869388.raw

```

180      175      180      185
182 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
183 190      195      200      205
185 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
186      210      215      220
188 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
189      225      230      235
191 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
192      240      245      250
194 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
195      255      260      265
197 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
E--> 198 270      275      280

```

620 &lt;210&gt; SEQ ID NO: 9

621 &lt;211&gt; LENGTH: 1459

622 &lt;212&gt; TYPE: DNA

623 &lt;213&gt; ORGANISM: homo sapiens

625 &lt;220&gt; FEATURE:

626 &lt;221&gt; NAME/KEY: CDS

627 &lt;222&gt; LOCATION: (309)..(989)

629 &lt;220&gt; FEATURE:

630 &lt;221&gt; NAME/KEY: sig\_peptide

631 &lt;222&gt; LOCATION: (309)..(359)

633 &lt;220&gt; FEATURE:

634 &lt;221&gt; NAME/KEY: mat\_peptide

635 &lt;222&gt; LOCATION: (360)..(986)

637 &lt;400&gt; SEQUENCE: 9

```

638 ggcacgacgc cccatctcta ctaataaaaa aaaaaaaaaa ggatttgaag tcctggccgg 60
640 agcaattagg caagggataa aaaggcacct aaggcccttt tgcaataaga agccagatgg 120
642 ataaaggaag tgctggtcac cctggaagtg tactggtttg gggaaggtcc ccggcccca 180
644 cagccctctg gggagcctca ccctggctct cccactcac ctcagccctc aggcagcccc 240
646 tccacaggac cctctcctg cctggacagc ttgctgggtc tccccgtccc ctggagaaga 300
648 acaaggcc atg ggt cgg ccc ctg ctg ctg ccc ctg ctg ctc ctg ctg cag 350
649 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Leu Leu Leu Gln
650 -15 -10 -5
652 ccg cca gca ttt ctg cag cct ggt ggc tcc aca gga tct ggt cca agc 398
653 Pro Pro Ala Phe Leu Gln Pro Gly Gly Ser Thr Gly Ser Gly Pro Ser
654 -1 1 5 10
656 tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg ggt 446
657 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly
658 15 20 25
660 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 494
661 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala
662 30 35 40 45
664 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 542
665 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly
666 50 55 60
668 cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat gtg 590
669 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val

```

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/869,388

DATE: 11/02/2001  
TIME: 14:45:23

Input Set : A:\es.txt  
Output Set: N:\CRF3\11022001\I869388.raw

```

670          65          70          75
672 aac cgg ctc ttt ctg aac tgg aca gag ggt cag gag agc ggc ttc ctc 638
673 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu
674          80          85          90
678 agg atc tca aac ctg cgg aag gag gac cag tct gtg tat ttc tgc cga 686
679 Arg Ile Ser Asn Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg
680          95          100          105
682 gtc gag ctg gac acc cgg aga tca ggg agg cag cag ttg cag tcc atc 734
683 Val Glu Leu Asp Thr Arg Arg Ser Gly Arg Gln Gln Leu Gln Ser Ile
684 110          115          120          125
686 aag ggg acc aaa ctc acc atc acc cag gct gtc aca acc acc acc acc 782
687 Lys Gly Thr Lys Leu Thr Ile Thr Gln Ala Val Thr Thr Thr Thr Thr
688          130          135          140
690 tgg agg ccc agc agc aca acc acc ata gcc ggc ctc agg gtc aca gaa 830
691 Trp Arg Pro Ser Ser Thr Thr Thr Ile Ala Gly Leu Arg Val Thr Glu
692          145          150          155
694 agc aaa ggg cac tca gaa tca tgg cac cta agt ctg gac act gcc atc 878
695 Ser Lys Gly His Ser Glu Ser Trp His Leu Ser Leu Asp Thr Ala Ile
696          160          165          170
698 agg gtt gca ttg gct gtc gct gtg ctc aaa act gtc att ttg gga ctg 926
699 Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val Ile Leu Gly Leu
700          175          180          185
702 ctg tgc ctc ctc ctg tgg tgg agg aga agg aaa ggt agc agg gcg cca 974
703 Leu Cys Leu Leu Leu Trp Trp Arg Arg Arg Lys Gly Ser Arg Ala Pro
704 190          195          200          205
E--> 706 agc agt gac ttc tga ccaacagagt gtggggagaa gggatgtgta ttagccccgg
707 1029
708 Ser Ser Asp Phe
E--> 711 aggacgtgat gtgagacccg cttgtgagtc ctccacactc gttccccatt ggcaagatac
712 1089
E--> 714 atggagagca ccctgaggac ctttaaaagg caaagccgca aggcagaagg aggctgggtc
715 1149
E--> 717 cctgaatcac cgactggagg agagttacct acaagagcct tcatccagga gcatccacac
718 1209
E--> 720 tgcaatgata taggaatgag gtctgaactc cactgaatta aaccactggc atttgggggc
721 1269
E--> 723 tgttcattat agcagtgcaa agagttcctt tatcctcccc aaggatggaa aatacaattt
724 1329
E--> 726 attttgetta ccatacacc cttttctcct cgtccacatt ttccaatctg tatggtggct
727 1389
E--> 729 gtcttctatg gcagaagggt ttgggggaata aatagcgtga aatgctgctg aaaaaaaaaa
730 1449
E--> 732 aaaaaaaaaa
733 1459

```

wrapped text  
See error summary  
sheet, item 1

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/869,388

DATE: 11/02/2001

TIME: 14:45:24

Input Set : A:\es.txt

Output Set: N:\CRF3\11022001\I869388.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:18 M:280 W: Numeric Identifier already exists, <140> found multiple times  
L:18 M:281 W: Numeric Fields not Ordered, <140> not ordered!.  
L:18 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:19 M:280 W: Numeric Identifier already exists, <141> found multiple times  
L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:198 M:252 E: No. of Seq. differs, <211>LENGTH:Input:284 Found:303 SEQ:2  
L:706 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:1029 SEQ:9  
M:254 Repeated in SeqNo=9  
L:793 M:112 C: (48) String data converted to lower case,  
L:801 M:112 C: (48) String data converted to lower case,  
L:809 M:112 C: (48) String data converted to lower case,  
L:820 M:112 C: (48) String data converted to lower case,